

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: SCHLEGEL, C. Richard
JENSON, A. Bennett
GHIM, Shin-Je
- (ii) TITLE OF INVENTION: PAPILLOMAVIRUS VACCINES
- (iii) NUMBER OF SEQUENCES: 2
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
 - (B) STREET: P.O. Box 1404
 - (C) CITY: Alexandria
 - (D) STATE: Virginia
 - (E) COUNTRY: United States
 - (F) ZIP: 22313-1404
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/724,281
 - (B) FILING DATE: 01-OCT-1996
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 60/004,691
 - (B) FILING DATE: 02-OCT-1995
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Teskin, Robin L.
 - (B) REGISTRATION NUMBER: 35,030
 - (C) REFERENCE/DOCKET NUMBER: 010091-015
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (703) 836-6620
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(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 508 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met	Tyr	Asn	Val	Phe	Gln	Met	Ala	Val	Trp	Leu	Pro	Ala	Gln	Asn	Lys
1				5					10					15	
Phe	Tyr	Leu	Pro	Pro	Gln	Pro	Ile	Thr	Arg	Ile	Leu	Ser	Thr	Asp	Glu
			20					25					30		
Tyr	Val	Thr	Arg	Thr	Asn	Leu	Phe	Tyr	His	Ala	Thr	Ser	Glu	Arg	Leu
			35				40						45		

Leu Leu Val Gly His Pro Leu Phe Glu Ile Ser Ser Asn Gln Thr Val
 50 55 60
 Thr Ile Pro Lys Val Ser Pro Asn Ala Phe Arg Val Phe Arg Val Arg
 65 70 75 80
 Phe Ala Asp Pro Asn Arg Phe Ala Phe Gly Asp Lys Ala Ile Phe Asn
 85 90 95
 Pro Glu Thr Glu Arg Leu Val Trp Gly Leu Arg Gly Ile Glu Ile Gly
 100 105 110
 Arg Gly Gln Pro Leu Gly Ile Gly Ile Thr Gly His Pro Leu Leu Asn
 115 120 125
 Lys Leu Asp Asp Ala Glu Asn Pro Thr Asn Tyr Ile Asn Thr His Ala
 130 135 140
 Asn Gly Asp Ser Arg Gln Asn Thr Ala Phe Asp Ala Lys Gln Thr Gln
 145 150 155 160
 Met Phe Leu Val Gly Cys Thr Pro Ala Ser Gly Glu His Trp Thr Ser
 165 170 175
 Arg Arg Cys Pro Gly Glu Gln Val Lys Leu Gly Asp Cys Pro Arg Val
 180 185 190
 Gln Met Ile Glu Ser Val Ile Glu Asp Gly Asp Met Met Asp Ile Gly
 195 200 205
 Phe Gly Ala Met Asp Phe Ala Ala Leu Gln Gln Asp Lys Ser Asp Val
 210 215 220
 Pro Leu Asp Val Val Gln Ala Thr Cys Lys Tyr Pro Asp Tyr Ile Arg
 225 230 235 240
 Met Asn His Glu Ala Tyr Gly Asn Ser Met Phe Phe Phe Ala Arg Arg
 245 250 255
 Glu Gln Met Tyr Thr Arg His Phe Phe Thr Arg Gly Gly Ser Val Gly
 260 265 270
 Asp Lys Glu Ala Val Pro Gln Ser Leu Tyr Leu Thr Ala Asp Ala Glu
 275 280 285
 Pro Arg Thr Thr Leu Ala Thr Thr Asn Tyr Val Gly Thr Pro Ser Gly
 290 295 300
 Ser Met Val Ser Ser Asp Val Gln Leu Phe Asn Arg Ser Tyr Trp Leu
 305 310 315 320
 Gln Arg Gly Gln Gly Gln Asn Asn Gly Ile Gly Trp Arg Asn Gln Leu
 325 330 335
 Phe Ile Thr Val Gly Asp Asn Thr Arg Gly Thr Ser Leu Ser Ile Ser
 340 345 350
 Met Lys Asn Asn Ala Ser Thr Thr Tyr Ser Asn Ala Asn Phe Asn Asp
 355 360 365
 Phe Leu Arg His Thr Glu Glu Phe Asp Leu Ser Phe Ile Val Gln Leu
 370 375 380
 Cys Lys Val Lys Leu Thr Pro Glu Asn Leu Ala Tyr Ile His Thr Met
 385 390 395 400

295 Asp Pro Asn Ile Leu Glu Asp Trp Gln Leu Ser Val Ser Gln Pro Pro
 405 410 415
 Thr Asn Pro Leu Glu Asp Gln Tyr Arg Phe Leu Gly Ser Ser Leu Ala
 420 425 430
 Ala Lys Cys Pro Glu Gln Ala Pro Pro Glu Pro Gln Thr Asp Pro Tyr
 435 440 445
 Ser Gln Tyr Lys Phe Trp Glu Val Asp Leu Thr Glu Arg Met Ser Glu
 450 455 460
 Gln Leu Asp Gln Phe Pro Leu Gly Arg Lys Phe Leu Tyr Gln Ser Gly
 465 470 475 480
 Met Thr Gln Arg Thr Ala Thr Ser Ser Thr Thr Lys Arg Lys Thr Val
 485 490 495
 Arg Val Ser Thr Ser Ala Lys Arg Arg Arg Lys Ala
 500 505

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 503 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Ala Val Trp Leu Pro Ala Gln Asn Lys Phe Tyr Leu Pro Pro Gln
 1 5 10 15
 Pro Ser Thr Lys Val Leu Ser Thr Asp Glu Tyr Val Ser Arg Thr Asn
 20 25 30
 Ile Phe Tyr His Ala Ser Ser Glu Arg Leu Leu Thr Val Gly His Pro
 35 40 45
 Phe Tyr Glu Ile Tyr Lys Glu Glu Arg Ser Glu Glu Val Ile Val Pro
 50 55 60
 Lys Val Ser Pro Asn Gln Tyr Arg Val Phe Arg Leu Leu Leu Pro Asp
 65 70 75 80
 Pro Asn Asn Phe Ala Phe Gly Asp Lys Ser Leu Phe Asp Pro Glu Lys
 85 90 95
 Glu Arg Leu Val Trp Gly Leu Arg Gly Leu Glu Ile Gly Arg Gly Gln
 100 105 110
 Pro Leu Gly Ile Ser Val Thr Gly His Pro Thr Phe Asp Arg Tyr Asn
 115 120 125
 Asp Val Glu Asn Pro Asn Lys Asn Leu Ala Gly His Gly Gly Gly Thr
 130 135 140
 Asp Ser Arg Val Asn Met Gly Leu Asp Pro Lys Gln Thr Gln Met Phe
 145 150 155 160
 Met Ile Gly Cys Lys Pro Ala Leu Gly Glu His Trp Ser Leu Thr Arg
 165 170 175

Trp Cys Thr Gly Gln Val His Thr Ala Gly Gln Cys Pro Pro Ile Glu
 180 185 190
 Leu Arg Asn Thr Thr Ile Glu Asp Gly Asp Met Val Asp Ile Gly Phe
 195 200 205
 Gly Ala Met Asp Phe Lys Ala Leu Gln His Tyr Lys Ser Gly Val Pro
 210 215 220
 Ile Asp Ile Val Asn Ser Ala Cys Lys Tyr Pro Asp Tyr Leu Lys Met
 225 230 235 240
 Ala Asn Glu Pro Tyr Gly Asp Arg Cys Phe Phe Phe Val Arg Arg Glu
 245 250 255
 Gln Leu Tyr Ala Arg His Ile Met Ser Arg Ser Gly Thr Gln Gly Leu
 260 265 270
 Glu Pro Val Pro Lys Asp Thr Tyr Ala Thr Arg Glu Asp Asn Asn Ile
 275 280 285
 Gly Thr Thr Asn Tyr Phe Ser Thr Pro Ser Gly Ser Leu Val Ser Ser
 290 295 300
 Glu Gly Gln Leu Phe Asn Arg Pro Tyr Trp Ile Gln Arg Ser Gln Gly
 305 315 320
 Lys Asn Asn Gly Ile Ala Trp Gly Asn Gln Leu Phe Leu Thr Val Val
 325 330 335
 Asp Asn Thr Arg Gly Thr Pro Leu Thr Ile Asn Ile Gly Gln Gln Asp
 340 345 350
 Lys Pro Glu Glu Gly Asn Tyr Val Pro Ser Ser Tyr Arg Thr Tyr Leu
 355 360 365
 Arg His Val Glu Glu Tyr Glu Val Ser Ile Ile Val Gln Leu Cys Lys
 370 375 380
 Val Lys Leu Ser Pro Glu Asn Leu Ala Ile Ile His Thr Met Asp Pro
 385 390 395 400
 Asn Ile Ile Glu Asp Trp His Leu Asn Val Thr Pro Pro Ser Gly Thr
 405 410 415
 Leu Asp Asp Thr Tyr Arg Tyr Ile Asn Ser Leu Ala Thr Lys Cys Pro
 420 425 430
 Thr Asn Ile Pro Pro Lys Thr Asn Val Asp Pro Phe Arg Asp Phe Lys
 435 440 445
 Phe Trp Glu Val Asp Leu Lys Asp Lys Met Thr Glu Gln Leu Asp Gln
 450 455 460
 Thr Pro Leu Gly Arg Lys Phe Leu Phe Gln Thr Asn Val Leu Arg Arg
 465 470 475 480
 Arg Ser Val Lys Val Arg Ser Thr Ser His Val Ser Val Lys Arg Lys
 485 490 495
 Ala Val Lys Arg Lys Arg Lys
 500